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Research Article

Two new *Periconia* species (Pleosporales, Ascomycota) in China

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Abstract

During an investigation of fungal diversity in Guangxi and Yunnan provinces, two interesting hyphomycetes were collected and isolated. Based on morphology, these hyphomycetes were similar to *Periconia*-like taxa. To confirm their classification, morphological characterization and multigene phylogenetic inference (using LSU, ITS, SSU, and *tef*1-α) were employed. Based on phylogenetic analyses, our two collections clustered within *Periconia* (Periconiaceae) as distinct two taxa, and morphological analyses also confirmed that they are new species of *Periconia*. *Periconia guangxiense* **sp. nov.** formed a well-supported monophyletic lineage (92% ML/1.00 PP) sister to *P. variicolor*, but morphologically, it is distinguishable by its branched, micronematous to semi-macronematous conidiophores. While *Periconia xishuangbannaensis* **sp. nov.** formed a distinct lineage closely related to *P. guangxiense*; it is distinguished by its macronematous conidiophores and dark brown conidia. This study highlights the role of unique habitats in driving fungal diversity and contributes to the taxonomic refinement of the *Periconia* genus.

Key words: 2 new species, biodiversity, fungal taxonomy, *Periconia guangxiense*, *Periconia xishuangbannaensis*

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Introduction

Periconiaceae was established by Nannizzi (1934) with *Periconia* as the type genus. Historically, Periconiaceae has long been neglected, and *Periconia* was included in Massarinaceae (Zhang et al. 2009; Hyde et al. 2013). Periconiaceae was formally established and placed in Pleosporales (Dothideomycetes) by Tanaka et al. (2015) based on phylogenetic analyses. Periconiaceae includes four accepted genera: *Bambusistroma*, *Flavomyces*, *Noosia*, and *Periconia*, along with a single lineage of "*Sporidesmium tengii*" (Tanaka et al. 2015). In the phylogenetic analyses, *Bambusistroma*, *Flavomyces*, *Noosia*, and *Sporidesmium tengii* were present in the *Periconia* lineage (Tanaka et al. 2015; Liu et al. 2017). Recent taxonomic revisions have synonymized *Bambusistroma* and *Noosia*

with *Periconia* (Tian et al. 2022; Yang et al. 2022), while *Flavomyces* remains a monotypic genus within the *Periconia* clade due to insufficient morphological characterization (Knapp et al. 2015; Tian et al. 2022).

Periconia was first described by Tode (1791) with *P. lichenoides* as the type species. Phylogenetic analyses by Tanaka et al. (2015) confirmed its placement in Periconiaceae, distinct from Massarinaceae. *Periconia* has 238 epithets listed in Index Fungorum (http://www.indexfungorum.org/; accessed August 20, 2025). Among these, 29 species have been transferred to other genera (Tian et al. 2022; Yang et al. 2022). Most *Periconia* species are hyphomycetous, with only five reported sexual morphs: *P. didymosporum*, *P. homothallica*, *P. igniaria*, *P. prolifica*, and *P. pseudodigitata* (Tanaka et al. 2015; Su et al. 2023; Liao et al. 2024). Asexual morphs are characterized by macronematous to micronematous, branched or unbranched conidiophores with spherical apices, monoblastic or polyblastic conidiogenous cells, and catenate, spherical to subspherical, verruculose conidia (Liao et al. 2024; He et al. 2025). Sexual morphs feature globose, scattered or grouped, ascomata with 8-spored, fissitunicate or cylindrical asci, and hyaline, 1-septate, fusiform, smooth ascospores with an entire sheath (Tanaka et al. 2015).

Periconia species are globally distributed, predominantly in temperate and tropical regions (Numata et al. 1997; Kolomiets et al. 2008; Sarkar et al. 2019; Gunasekaran et al. 2021; Madagammana et al. 2024; He et al. 2025). They occupy diverse ecological roles as saprobes, endophytes, plant pathogens (e.g., *P. igniaria* causing leaf spots on yellow starthistle; Kolomiets et al. 2008), and rarely human pathogens (e.g., *P. keratitis* causing mycotic keratitis; Gunasekaran et al. 2021). Aquatic species, on the other hand, such as *P. aquatica* and *P. submersa* are less common (Dong et al. 2020; Shen et al. 2024; Hongsanan et al. 2025).

In this study, two fungal taxa were collected and isolated from submerged decaying wood in a river and on dead leaves of *Zea mays* in Guangxi and Yunnan provinces. Multilocus phylogenetic analyses of combined LSU, ITS, SSU, and *tef*1-α sequence data placed them in *Periconia*. This study describes two new taxa, *Periconia guangxiense* and *P. xishuangbannaensis*, with detailed descriptions and illustrations. The research enhances our understanding of the ecological roles that *Periconia* species play in their respective environments and supports ongoing efforts to map the extensive fungal diversity present in unique habitats in China.

Materials and methods

Sample collection, isolation, and morphological examination

Specimens were collected from submerged decaying wood in a Guangxi freshwater stream and dead *Zea mays* leaves in Guangxi and Yunnan provinces, China (Tian et al. 2024). Samples were tagged with the collection information (Rathnayaka et al. 2025), put in sterile zip-lock bags, and taken to the mycology laboratory for processing. Single-spore isolation and morphological observations followed the methods of Senanayake et al. (2020). Morphological characteristics were examined using a stereomicroscope (Motic SMZ-171, Wetzlar, Germany). Microstructures were photographed with a Nikon DS-Ri2 camera mounted on a Nikon ECLIPSE Ni-U microscope (New York, USA). Measurements were taken using Image Framework v.0.9.0.7, and images processed with Adobe Photoshop CS6 (Adobe Systems, San Jose, CA, USA) (Tian et al. 2024).

Specimens were deposited in the herbarium of Guizhou Academy of Agriculture Sciences (GZAAS), Guiyang, China, while living cultures were deposited in the Guizhou Culture Collection (GZCC), Guiyang, China. The Index Fungorum (IF) number for the new species was obtained from Index Fungorum (2025). The new taxon was established according to the guidelines outlined by Jeewon (2016) and Chethana et al. (2021).

DNA extraction, PCR amplification, and sequencing

Genomic DNA was extracted from 2-week-old pure cultures using a BioFlux BSC14S1 kit (Hangzhou, China) following the manufacturer's instructions. The genomic DNA was stored at 4 °C and subjected to polymerase chain reaction (PCR) to amplify partial gene regions using the following primers: the partial large subunit nuclear rDNA (LSU) with primer pairs LR0R/LR5 (Vilgalys and Hester 1990), the internal transcribed spacer (ITS) gene was amplified with primer pairs ITS4/ITS5 (White et al. 1990), SSU gene was amplified using primers NS1 and NS4 (White et al. 1990).

The PCR amplifications were carried out using LSU, ITS, and SSU following the method described by Tian et al. (2024). The PCR thermal cycle programs for LSU, ITS, and SSU were as follows: an initialization step of 95 °C for 4 min, followed by 35 cycles of 94 °C for 40 s, an annealing step at 55 °C for 55 s, an elongation step at 72 °C for 50 min and a final extension step of 72 °C for 10 min. PCR products were checked on 1% agarose gels and sequenced using the same primers by Sangon Biotech Co., Kunming, China.

Phylogenetic analyses

Forward and reverse sequences were assembled with SeqMan and subjected to BLASTn in NCBI (https://blast.ncbi.nlm.nih.gov/Blast.cgi) to identify the most similar taxa. Sequences of Periconiaceae were retrieved from GenBank (https://www.ncbi.nlm.nih.gov/) based on recent publications (Bao et al. 2025; He et al. 2025; Sun et al. 2025) and are listed in Table 1. Single gene sequence alignment was generated with the MAFFT v.7 online program (http://mafft.cbrc.jp/alignment/server/, 22 January 2025; Katoh and Standley 2013), trimmed using trimAl v 1.2 (Capella-Gutiérrez et al. 2009) and concatenated using Sequence Matrix. The FASTA alignment formats were changed to PHYLIP (for RAxML) and NEXUS formats (for BI) by Aliview 2.11. Multigene phylogenetic analyses were conducted using maximum likelihood (ML) and Bayesian inference (BI).

Maximum likelihood analysis was done by the online RAxML-HPC v.8 on XSEDE Teragrid on CIPRES Science Gateway V. 3.3 (https://www.phylo.org, 22 August 2025) using the GTRGAMMA substitution model with 1,000 bootstrap replicates (Stamatakis et al. 2008; Miller et al. 2010; Dissanayake et al. 2020). The final tree was selected from suboptimal trees from each run by comparing likelihood scores.

Bayesian inference analysis was performed using MrBayes v. 3.2 on the XSEDE tool on the CIPRES portal (Miller et al. 2010). The models were selected as GTR+I+G for LSU, SSU, ITS, and *tef*1-α gene regions based on the best-fit model for BI analysis, which was estimated using MrModeltest v. 2.2 (Nylander 2004). Posterior probabilities (PP) (Rannala and Yang 1996; Zhaxybayeva

and Gogarten 2002) were defined by the Bayesian Markov chain Monte Carlo (BMCMC) sampling method in MrBayes v.3.0b4 (Rannala and Yang 1996; Huelsenbeck and Ronquist 2001; Zhaxybayeva and Gogarten 2002). Two parallel runs were conducted using the default settings; six simultaneous Markov chains were run for 5,000,000 generations, and trees were sampled every 500th generation. Phylogenetic trees were visualized using FigTree v1.4.4 (Rambaut 2012), and layouts were created with Adobe Illustrator CS5 v. 16.0.0 and Adobe Photoshop 2021 software (Adobe Systems, California, USA). All newly generated sequences were deposited in GenBank (https://www.ncbi.nlm.nih.gov/).

Genealogical concordance phylogenetic species recognition (GCPSR) analysis

The genealogical concordance phylogenetic species recognition analysis is a model test used to check significant recombinant events (Tian et al. 2024). The data were analyzed using SplitsTree V4 with the pairwise homoplasy index (PHI) test to estimate recombination levels among closely related species (Bruen et al. 2006). A multilocus concatenated dataset with closely related species was used for the analysis. The relationships between closely related taxa were visualized by constructing split graphs using the LogDet transformation and splits decomposition options. PHI results below a 0.05 threshold ($\Phi w < 0.05$) indicate significant recombination in the dataset.

Table 1. Taxon names, strain numbers, and GenBank accession numbers of the fungal taxa used in this study.

Species name	Strain/ voucher NO.	GenBank accession numbers			
		ITS	LSU	SSU	*tef*1-α
Bambusistroma didymosporum	MFLU 15-0058	KP761734	KP761731	KP761738	KP761728
Flavomyces fulophazii	**CBS 135761**	**NR_137960**	**NG_058131**	**NG_061191**	**/**
Flavomyces fulophazii	CBS 135664	KP184000	KP184039	KP184081	/
Lentithecium aquaticum	**CBS 123099**	**NR_160229**	**NG_064211**	**NG_016507**	**GU349068**
Lentithecium clioninum	**KT1149A**	**LC014566**	**AB807540**	**AB797250**	**AB808515**
Lentithecium clioninum	KT1220	LC014567	AB807541	AB797251	AB808516
Massarina cisti	**CBS 266.62**	**/**	**AB807539**	**AB797249**	**AB808514**
Massarina eburnea	CBS473.64	/	GU301840	GU296170	GU349040
Morosphaeria ramunculicola	KH220	/	AB807554	AB797264	AB808530
Moroxphaeria velatispora	KH221	LC014572	AB807556	AB797266	AB808532
Periconia algeriana	**CBS 321.79**	**MH861212**	**MH872979**	/	/
Periconia alishanica	**NCYU 19-0160**	**MW063165**	**MW063229**	/	**MW183790**
Periconia ananasi	**MFLUCC 21-0155**	**OL753685**	**OL606153**	**OL606142**	**OL912946**
Periconia aquatica	**MFLUCC 16-0912**	**KY794701**	**KY794705**	/	**KY814760**
Periconia arecacearum	**MFLU 19-0803**	**PP592462**	**PP621090**	**PP639222**	**PP828795**
Periconia arecacearum	**SNT19A**	**PP592462**	**PP621090**	**PP639222**	**PP828795**
Periconia artemisiae	**KUMCC 20-0265**	**MW448657**	**MW448571**	**MW448658**	**MW460898**
Periconia atropurpurea	**CBS 381.55**	**MH857524**	**MH869061**	/	/
Periconia banksiae	**CBS 129526**	**/**	**NG_064279**	**/**	**/**
Periconia byssoides	MFLUCC 18-1548	MK347794	MK348013	MK347902	MK360070
Periconia byssoides	MFLUCC 17-2292	MK347751	MK347968	MK347858	MK360069
Periconia byssoides	MAFF 243869	LC014582	AB807569	AB797279	AB808545
Periconia byssoides	MFLUCC 18-1553	MK347806	MK348025	MK347914	MK360068

Species name	Strain/ voucher NO.	GenBank accession numbers			
		ITS	LSU	SSU	*tef*1-α
Periconia caespitosa	TC-2018a	MH051906	MH051907	/	/
Periconia calamagrostidicola	**CBS150887**	**PP791432**	**PP791460**	/	**PP780620**
Periconia celtidis	MFLU 19-2784	MW063162	MW063226	/	/
Periconia chengduensis	**CGMCC 3.23930**	**OP955987**	**OP956012**	**OP956056**	**OP961453**
Periconia chiangraiensis	**MFLUCC 21-0164**	**OL753686**	**OL606154**	**OL606143**	**OL912947**
Periconia chimonanthi	**KUMCC 20-0266**	**MW448660**	**MW448572**	**MW448656**	**MW460897**
Periconia circinata	CBS 263.37	MW810265	MH867413	/	MW735660
Periconia citlaltepetlensis	**IOM 325319**	**MH890645**	**MT625978**	/	/
Periconia cookei	MFLUCC 17-1399	MG333490	MG333493	/	MG438279
Periconia cookei	MFLUCC 17-1679	/	MG333492	/	MG438278
Periconia cortaderiae	MFLUCC 15-0453	KX965733	KX954402	/	KY320574
Periconia cortaderiae	**MFLUCC 15-0457**	**KX965732**	**KX954401**	**KX986345**	**KY310703**
Periconia cortaderiae	MFLUCC 15-0451	KX965734	KX954403	KX986346	KY429208
Periconia cynodontis	CGMCC 3.23927	OP909925	OP909921	OP909920	OP961434
Periconia cyperacearum	**CPC 32138**	**NR_160357**	**NG_064549**	/	/
Periconia delonicis	**MFLUCC 17-2584**	/	**NG_068611**	**NG_065770**	**MK360071**
Periconia digitata	CBS510.77	LC014584	AB807561	AB797271	AB808537
Periconia dujuanhuensis	**KUNCC 23-13482**	**PQ340469**	**PP189907**	/	**PQ456957**
Periconia elaeidis	**MFLUCC 170087**	**MG742713**	**MH108552**	**MH108551**	/
Periconia endophytica	**ZHKUCC 23-0995**	**OR995582**	**OR995588**	**PP277722**	**PP025968**
Periconia endophytica	ZHKUCC 23-0996	OR995583	OR995589	PP277723	PP025969
Periconia epilithographicola	**CBS 144017**	**NR_157477**	/	/	/
Periconia festucae	**CGMCC 3.23929**	**OP955973**	**OP955998**	**OP956042**	**OP961439**
Periconia floridana	**CBS 150884**	**NR_197917**	**NG_244042**	/	/
Periconia guangxiense	**GZAAS 25-0735**	**PX118886**	**PX118882**	**PX118890**	**PX522310**
Periconia guangxiense	GZAAS 25-0733	PX118887	PX118883	PX118891	PX522311
Periconia genistae	**CBS 322.79**	**MH861213**	**MH872980**	/	/
Periconia homothallica	**KT916**	**AB809645**	**AB807565**	**AB797275**	/
Periconia hongheensis	**KUNCC 23-13550**	**PQ340467**	**PP189905**	/	**PQ456958**
Periconia hydei	ZHKUCC 24-2102	PV434172	PV436641	PV437587	PV588048
Periconia hydei	**ZHKUCC 24-2101**	**PV434171**	**PV436640**	**PV437586**	**PV588047**
Periconia igniaria	CBS 379.86	LC014585	AB807566	AB797276	AB808542
Periconia igniaria	CBS 845.96	LC014586	AB807567	AB797277	AB808543
Periconia imperatae	**CGMCC 3.23931**	**OP955984**	**OP956009**	**OP956053**	**OP961450**
Periconia kunmingensis	**KUMCC 18-0173**	**MH892346**	**MH892399**	**OR225814**	**MH908963**
Periconia lateralis	CBS 292.36	MH855804	MH867311	/	/
Periconia linzhiensis	**HKAS 144526**	**PQ684989**	**PQ675408**	**PQ675368**	**PQ671465**
Periconia macrospinosa	CBS 135663	KP183999	KP184038	KP184080	/
Periconia macrospinosa	REF144	JN859364	JN859484	/	/
Periconia minutissima	MFLUCC 15-0245	KY794703	KY794707	/	/
Periconia minutissima	MUT2887	MG813227	/	/	/
Periconia motuoensis	**KUNCC24-17924**	**PQ373177**	**PQ438054**	**PQ438116**	**PQ661220**
Periconia muchuanensis	**CGMCC 3.25599**	**PQ067868**	**PQ067698**	**PQ066546**	**PQ278553**
Periconia neobrittanica	**CPC 37903**	**NR_166344**	**NG_068342**	/	/
Periconia neominutissima	**CBS 149514**	**OQ628478**	**OQ629060**	/	**OQ627950**
Periconia palmicola	**MFLUCC 14-0400**	/	**NG_068917**	**MN648319**	**MN821070**
Periconia penniseti	**CGMCC 3.23928**	**OP955971**	**OP955996**	**OP956040**	**OP961437**
Periconia philadelphiana	**CBS 149681**	**OQ628486**	**OQ629068**	/	**OQ627953**
Periconia prolifica	DBOF129	JQ724490	/	/	/
Periconia prolifica	DBOF23	JQ724384	/	/	/

Species name	Strain/ voucher NO.	GenBank accession numbers			
		ITS	LSU	SSU	*tef*1-α
Periconia prolifica	DBOF74	JQ724435	/	/	/
Periconia prolifica	DBOF153	JQ724513	/	/	/
Periconia prolifica	**CBS 209.64T**	**MH858422**	**MH870050**	/	/
Periconia pseudobyssoides	MFLU 17-1970	MG333491	MG333494	/	MG438280
Periconia pseudobyssoides	MAFF 243868	LC014587	AB807568	AB797278	AB808544
Periconia pseudobyssoides	MAFF 243874	LC014588	AB807560	AB797270	AB808536
Periconia pseudodigitata	KT644	LC014589	AB807562	AB797272	AB808538
Periconia pseudodigitata	KT1195A	LC014590	AB807563	AB797273	AB808539
Periconia sahariana	**CBS 320.79**	**MW444854**	**MH872978**	/	/
Periconia salina	**MFLU 19-1235**	**MN047086**	**MN017846**	**MN017912**	/
Periconia shannanensis	HKAS 134943	PP968554	PP968557	PP968560	PQ226772
Periconia sichuanensis	**CGMCC 3.25598**	**PQ067867**	**PQ067697**	**PQ066545**	**PQ278551**
Periconia spodiopogonis	**CGMCC 3.23932**	**OP955963**	**OP955988**	**OP956032**	**OP961429**
Periconia submersa	**MFLUCC 16-1098**	**KY794702**	**KY794706**	/	**KY814761**
Periconia thailandica	**MFLUCC 17-0065**	**KY753887**	**KY753888**	**KY753889**	/
Periconia thysanolaenae	**KUMCC 20-0262**	**MW442967**	/	/	**MW460896**
Periconia variicolor	SACCR-64	DQ336713	/	/	/
Periconia variicolor	BHE4	OR269168	/	/	/
Periconia variicolor	isolate L5	OP881885	/	/	/
Periconia variicolor	isolate 39JAN	ON208681	/	/	/
Periconia variicolor	strain F5	MF170861	/	/	/
Periconia verrucosa	MFLUCC 17-2158	MT310617	MT214572	MT226686	MT394631
Periconia wurfbainiae	**ZHKUCC 23-0999**	**OR995586**	**OR995592**	**PP277726**	**PP025972**
Periconia wurfbainiae	ZHKUCC 23-1000	OR995587	OR995593	PP277727	PP025973
Periconia xishuangbannaensis	**GZAAS25-0707**	**PX118888**	**PX118884**	**PX118892**	**PX522312**
Periconia xishuangbannaensis	GZAAS25-0734	PX118889	PX118885	/	/
Periconia yangjiangensis	**ZHKUCC 23-0997**	**OR995584**	**OR995590**	**PP277724**	**PP025970**
Periconia yangjiangensis	ZHKUCC 23-0998	OR995585	OR995591	PP277725	PP025971
Periconia yantingense	**SICAUCC 23-0047**	**PP060663**	**PP057956**	**PP003824**	**PP061142**
Periconia yunnanensis	**KUNCC 23-14259**	**PQ340468**	**PP189906**	/	**PQ456960**

Notes: Newly-generated sequences are indicated in cells with light red shading. Type strains are indicated in black/bold with light red shading. The symbol "/" indicates sequence not available.

Results

Phylogenetic analyses

The combined LSU, ITS, SSU, and *tef*1-α dataset comprised 104 strains, including four newly sequenced strains, with *Morosphaeria ramunculicola* (KH220) and *M. velatispora* (KH221) as the outgroup taxa. Multiple genes were concatenated, comprising 3,458 nucleotide characters, including gaps in the ITS (1–568), LSU (569–1,481), SSU (1,482–2,508), and *tef*1-α (2,509–3,438) regions. The RAxML analysis of the combined dataset yielded the best-scoring tree (Fig. 1) with a final ML optimization likelihood value of -25425.074632. The matrix contained 1,486 distinct alignment patterns, with 30.78% of the characters being undetermined or gaps. Estimated base frequencies were as follows: A = 0.237622, C = 0.257752, G = 0.267613, T = 0.237014; substitution rates: AC = 1.661890, AG = 2.814269, AT = 1.647163, CG = 1.275088, CT = 9.578081, GT = 1.000000; gamma distribution shape parameter α = 0.265472.

In this study, our phylogenetic analyses yielded a topology similar to those reported in previous studies (Yang et al. 2022; Liao et al. 2024), and our isolates were placed within *Periconia* (Fig. 1). The new isolates (GZAAS 25-0733 and GZAAS 25-0735) formed an independent lineage basal to *Periconia variicolor* with 92% ML/1.00 PP bootstrap support, while the other new isolates (GZAAS 25-0707 and GZAAS 25-0734) formed a well-supported independent lineage within the

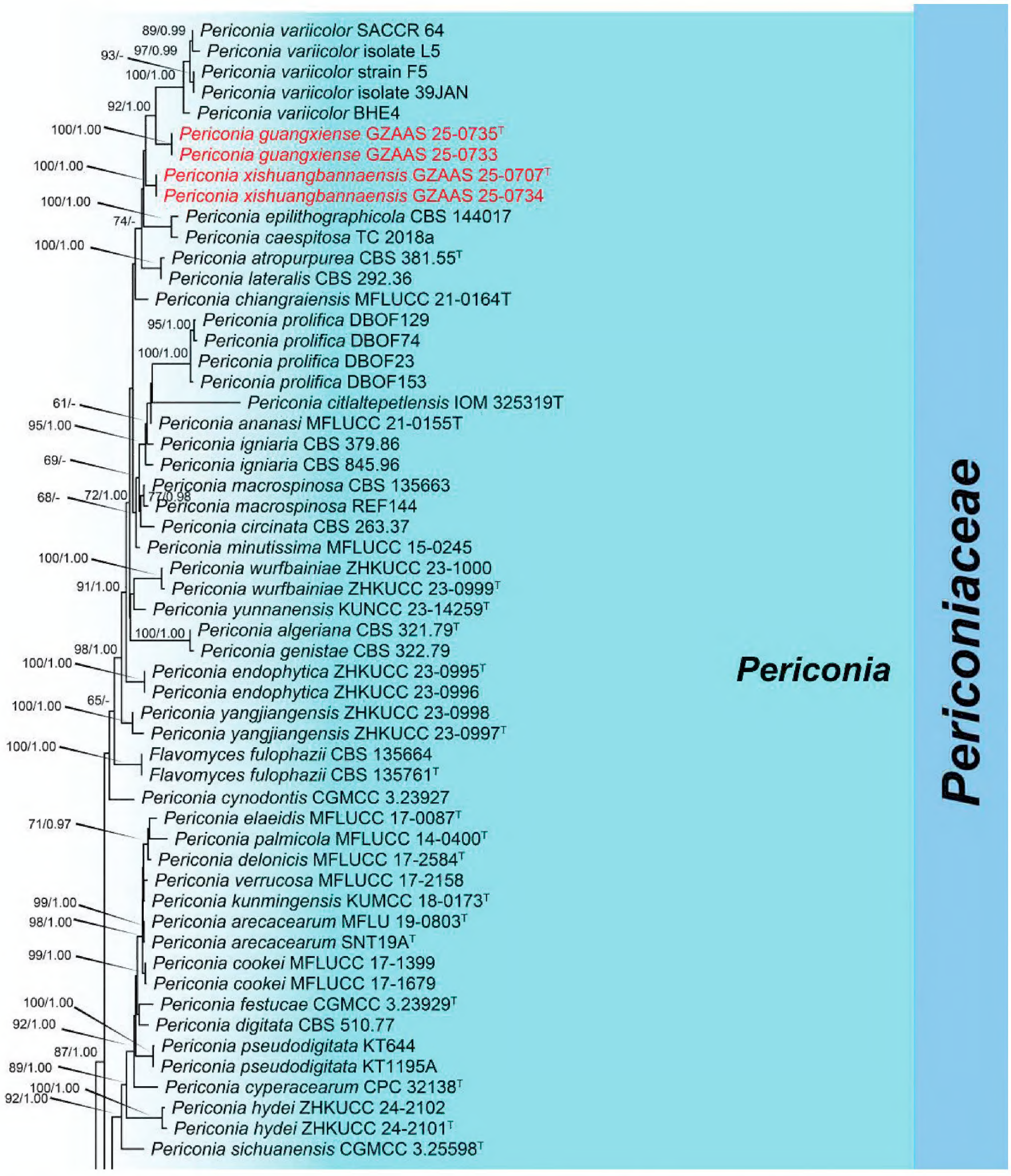

Figure 1. Phylogram generated from maximum likelihood (ML) analysis based on a concatenated alignment of ITS, LSU, SSU, and *tef*1-α sequences in Periconiaceae. Related sequences were obtained from Bao et al. (2025). The tree was rooted with *Morosphaeria ramunculicola* (KH220) and *M. velatispora* (KH221). Bootstrap support values for ML equal to or greater than 60% and clade credibility values greater than 0.90 from Bayesian inference analysis are labelled at each node. The new isolates are indicated in red, while "T" indicates holotype or ex-type strains.

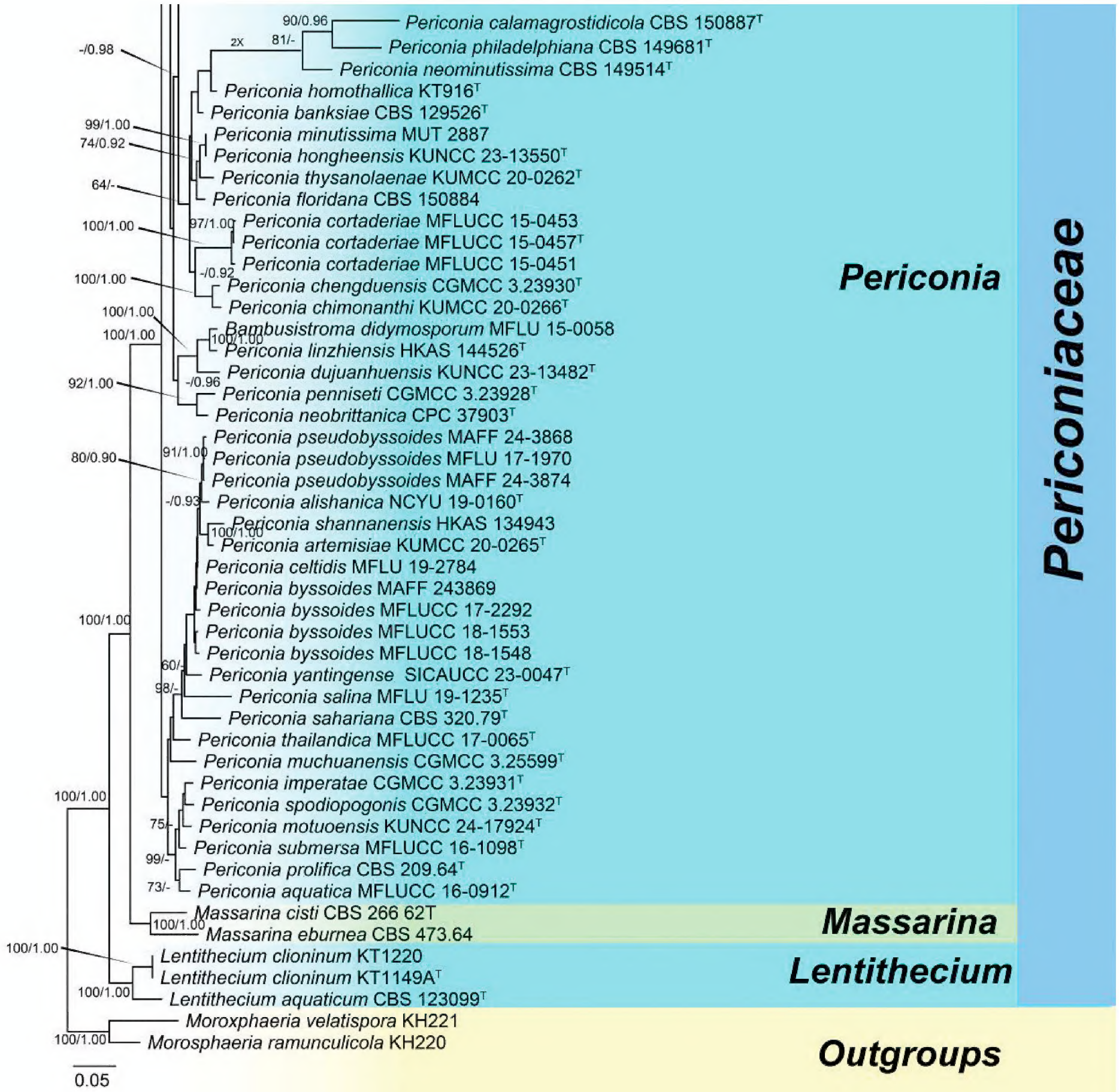

Figure 1. Continued.

genus with low statistical support. Additionally, other species of *Periconia* were well separated, whereas *Flavomyces fulophazii* clustered within *Periconia*, an observation similar to other trees (Knapp et al. 2015; Tian et al. 2022).

Taxonomy

***Periconia guangxiense* X.G. Tian & D.F. Bao, sp. nov.**

Index Fungorum number: IF904184

Fig. 2

Holotype. GZAAS 25-0735. The holotype GZAAS 25-0735 is the representative specimen of *Periconia guangxiense*, collected from decaying submerged wood in a freshwater stream in Longlin City, Guangxi Province, China, on 24 Novem-

ber 2024, by Dan-Feng Bao (collection code: NPJ 8-30/B199). This holotype specimen is deposited in the herbarium of Guizhou Academy of Agricultural Sciences (GZAAS) in Guiyang, China, while its corresponding ex-type living culture (GZCC 25-0705) is stored in the Guizhou Culture Collection (GZCC).

Etymology. Named after the type location, "Guangxi".

Description. ***Saprobic*** on decaying submerged wood in freshwater habitats. ***Sexual morph*** Undetermined. ***Asexual morph*** Hyphomycetous. ***Colonies*** effuse on natural substrate, scattered, hairy, dark brown to dark. ***Mycelium*** composed

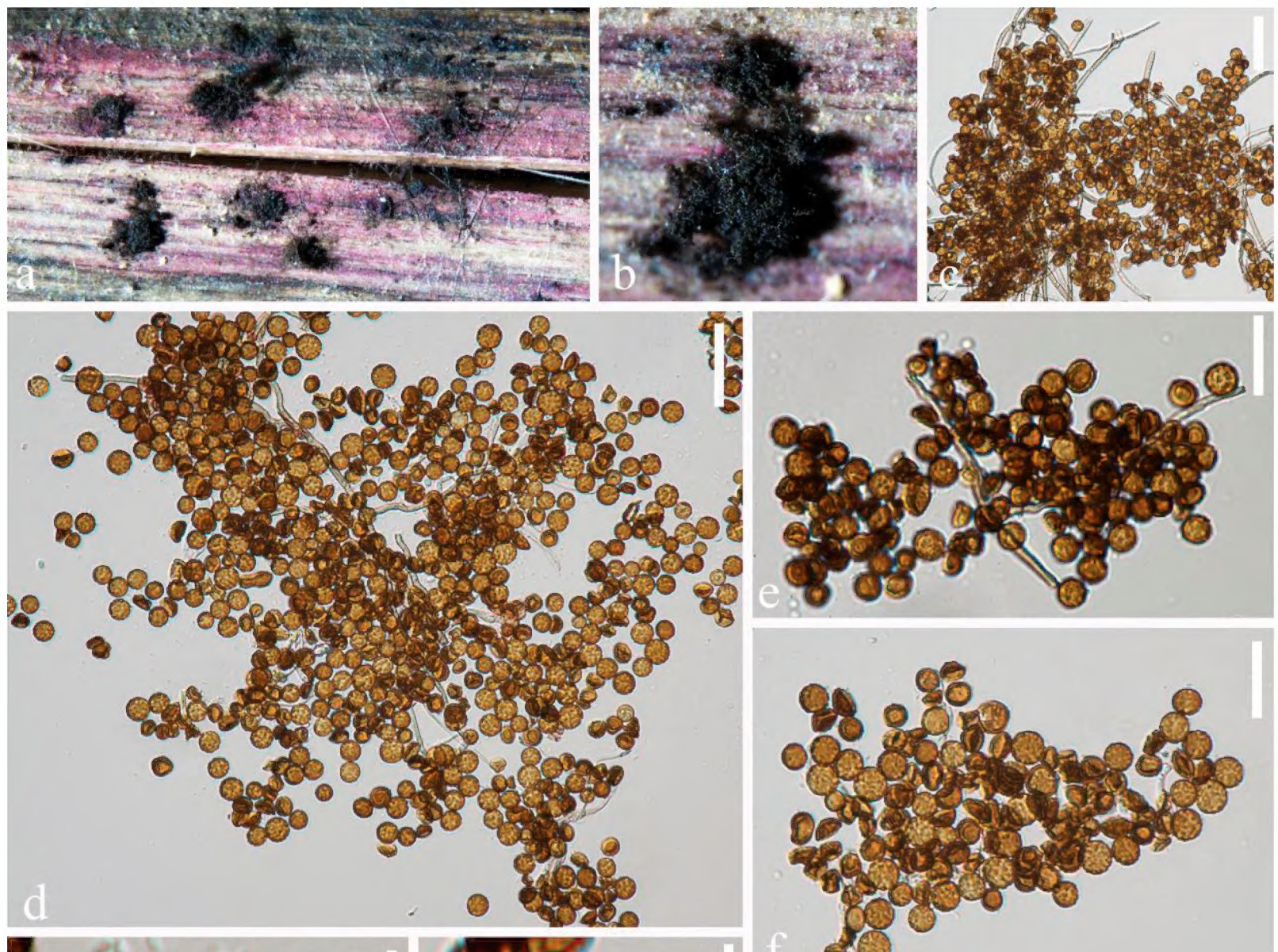

Figure 2. *Periconia guangxiense* (GZAAS25-0735, holotype). **a, b.** Colonies on submerged decaying wood; **c–f.** Conidial masses; **g–i.** Conidiogenous cells with conidia; **j–m.** Conidia; **n–o.** Culture on PDA from obverse and reverse view. Scale bars: 30 μm (**c–d**); 20 μm(**e–f**); 10 μm (**g–m**).

of cottony hyphae, forming dark clusters with conidia. ***Conidiophores*** micronematous to semi-macronematous, mononematous, branched, caespitose, straight or flexuous, hyaline when young, turning brown to dark brown, cylindrical, septate, smooth-walled. ***Conidiogenous cells*** 19–28 × 2.5–4.5 µm ($\bar{x}$ = 23 × 3.5 µm, n = 6), mono- to polyblastic, determinate, discrete on stipe, intercalary, smooth to minutely verruculose, ellipsoid to cylindrical, brown. ***Conidia*** 6–7.5 µm diam. ($\bar{x}$ = 6.8 µm, n = 60), subglobose to globose, aseptate, reddish-brown to dark brown, arising at one or more points on the curved surface of the conidiogenous cell, in branched chains, bud scars or disjunctors present at the site of attachment, verruculose.

Culture characteristics. Conidia germinated on PDA within 24 hr, reaching 20 mm diam. in 2 weeks at 25 °C. Colonies on PDA with white mycelia on the surface, cottony, circular, and flattened; reverse reddish brown with a pink margin, not sporulate on PDA after two weeks.

Material examined. CHINA • Guangxi Province, Longlin City, on decaying submerged wood, 24 Nov. 2024, D.F. Bao, NPJ 8-30 (B199) (GZAAS 25-0735, holotype), ex-type, GZCC 25-0705; *ibid.* NPJ 8-12 (GZAAS 25-0733, isotype), ex-isotype, GZCC 25-0704.

GenBank numbers. GZCC 25-0705: ITS = PX118886, LSU = PX118882, SSU = PX118890, tef1-α = PX522310; GZCC 25-0704: ITS = PX118887, LSU = PX118883, SSU = PX118891, tef1-α = PX522311.

Notes. In the phylogenetic analyses of the combined ITS, LSU, SSU, and *tef-1α* sequence data, our newly obtained strains of *Periconia guangxiense* (GZAAS 25-0735) formed a distinct lineage and clustered sister to *P. variicolor* strains (SACCR 64, isolate 5, F5, isolate 39JAN, BHE4) with 92% ML and 1.00 PP statistical supports (Fig. 1). Morphologically, *Periconia guangxiense* **(**GZAAS25-0735, holotype**)** can be easily distinguished from *P. variicolor* (CBS 120374) by micronematous, branched conidiophores, while *P. variicolor* has macronematous and unbranched conidiophores. *Periconia guangxiense* also has a smaller size range of conidia (6–7.5 µm vs. 7.5–9.5 µm) than the holotype of *P. variicolor* (CBS 120374) (Cantrell et al. 2007). In addition, pairwise nucleotide comparisons showed that ITS of *Periconia guangxiense* (GZCC 25-0705) differed 40/508 bp (7.87%, with gaps) from that of *P. variicolor* (SACCR-64), which strongly supports our strains as a new species. The PHI test revealed no significant recombination event between our strains (GZAAS25-0735 and GZAAS25-0733) and the closely related taxa. The significant recombination between our two strains indicates that they are conspecific (Φw = 0.98) (Fig. 4). Therefore, *Periconia guangxiense* is introduced as a distinct new species of *Periconia*.

Periconia xishuangbannaensis **X.G. Tian & D.F. Bao, sp. nov.**

Index Fungorum number: IF904185

Fig. 3

Holotype. GZAAS 25-0707. The holotype GZAAS 25-0707 is the representative specimen of *Periconia xishuangbannaensis*. It was collected from dead leaves of *Zea mays* in Xishuangbanna City, Yunnan Province, China, on September 17, 2021, by Xing-Guo Tian (collection code: corn3-2). This holotype specimen is deposited in the herbarium of Guizhou Academy of Agricultural Sciences

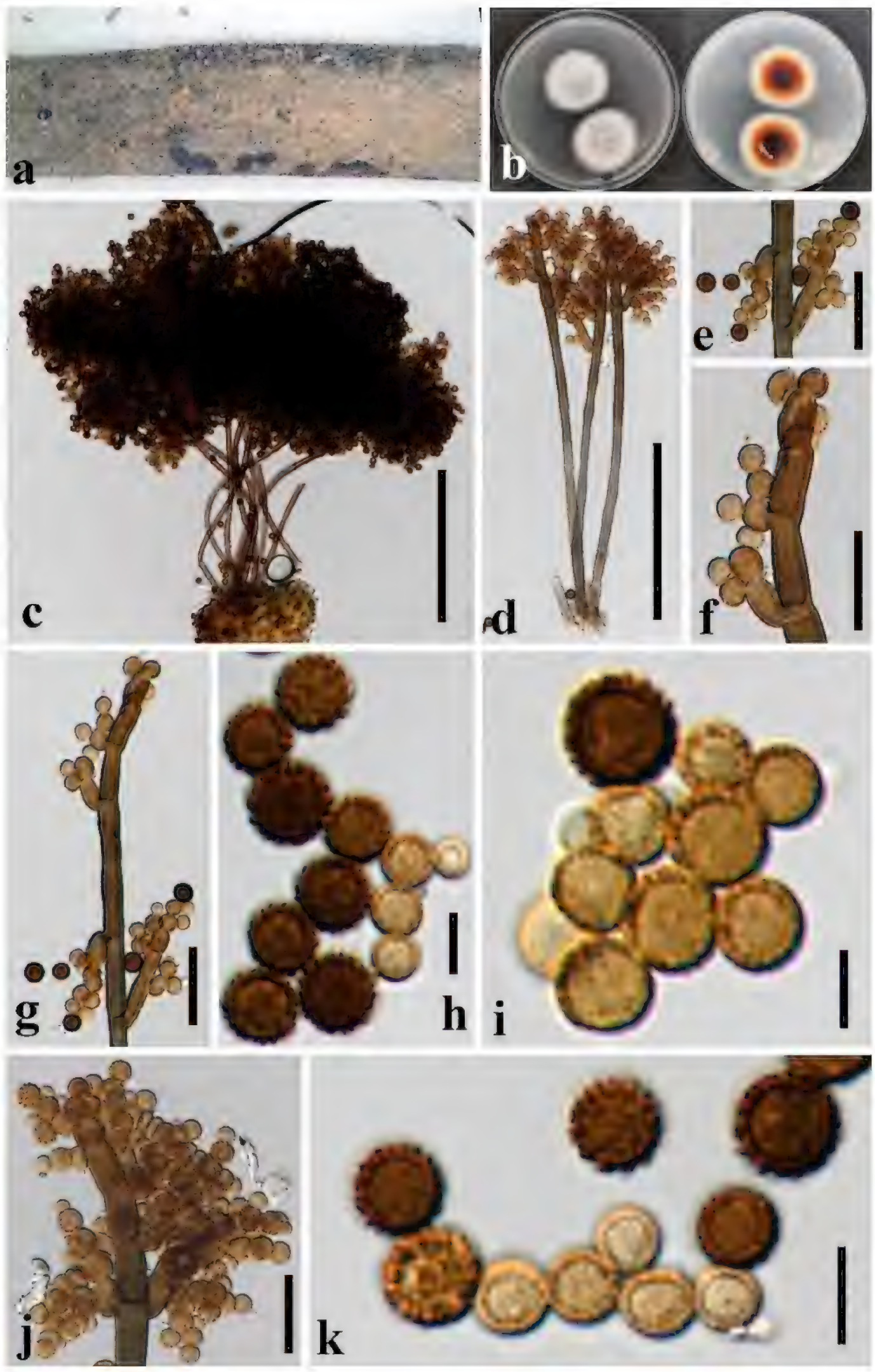

Figure 3. *Periconia xishuangbannaensis* (GZAAS 25-0707, holotype). **a.** Colonies on natural substrate; **b.** Colonies on PDA from above and below; **c–d.** Conidiophores, conidiogenous cells, and conidia; **e–g, j.** Conidiogenous cells and conidia; **h, i, k.** Conidia. Scale bars: 100 μm (**c–d**), 20 μm (**e–g, j**), 5 μm (**h, i, k**).

(GZAAS) in Guiyang, China, while its corresponding ex-type living culture (GZCC 25-0677) is stored in the Guizhou Culture Collection (GZCC).

Etymology. Named after the type location, "Xishuangbanna".

Description. ***Saprobic*** on dead leaves of corn. ***Sexual morph*** Undetermined. ***Asexual morph*** Hyphomycetous. ***Colonies*** effuse on the natural substrate, gregarious, dark brown to black, floccose, and spore masses spread on the host surface. ***Mycelium*** partly superficial, composed of septate, brown hyphae.

Conidiophores 229–247 × 4.5–7 µm ($\bar{x}$ = 243 × 5.5 µm, n = 5), macronematous, mononematous, caespitose, erect, cylindrical, straight or slightly flexuous, branched, septate, cylindrical, smooth, brown, smooth-walled. ***Conidiogenous cells*** 6.5–14 × 4–6 µm ($\bar{x}$ = 10 × 5 µm, n = 15), holoblastic, often polyblastic, terminal or intercalary, integrated, discrete on stipe, subcylindrical, smooth to verruculose, pale brown to brown. ***Conidia*** 4.5–7 µm ($\bar{x}$ = 6 µm, n = 30) diam., globose, aseptate, pale brown to brown, becoming dark brown at maturity, arising at one or more points on the curved surface of the conidiogenous cell, catenate, minutely verruculose to short-spinulose.

Culture characteristics. Conidia germinated on PDA within 24 hr, reaching 15 mm diam. in 2 weeks at 25 °C. Colonies on PDA with white mycelia on the surface, cottony, circular, and flattened; reverse of the colony is brown with a white margin, not sporulate in PDA after two weeks.

Material examined. CHINA • Yunnan Province, Xishuangbanna City, on dead leaves of *Zea mays*, 17 Sep. 2021, X.G. Tian, corn3-2 (GZAAS 25-0707 holotype), ex-type, GZCC 25-0677; *ibid.* corn3-13 (GZAAS 25-0734, isotype), ex-isotype, GZCC 25-0703.

GenBank numbers. GZCC 25-0677: ITS = PX118888, LSU = PX118884, SSU = PX118892, tef1-α = PX522312; GZCC 25-0703: ITS = PX118889, LSU = PX118885.

Notes. In the phylogenetic analyses of the combined ITS, LSU, SSU, and *tef*1-*α* sequence data, our newly obtained strains of *Periconia xishuangbannaensis* formed a distinct lineage and clustered as a sister clade to *P. variicolor* (SACCR-64) and *P. guangxiense* without statistical support (Fig. 1). Morphologically, *P. xishuangbannaensis* can be easily distinguished from *P. variicolor* by

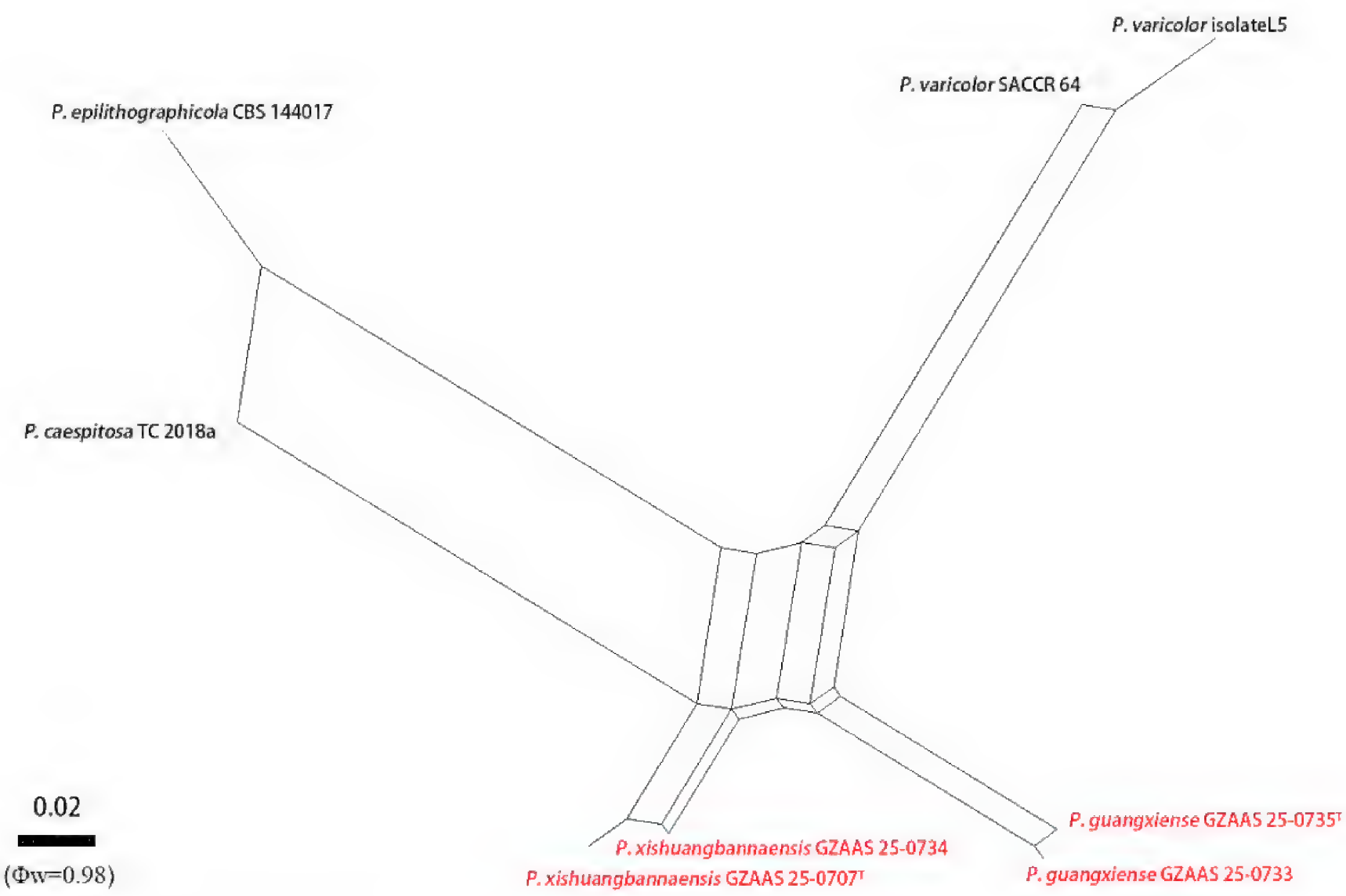

Figure 4. Results of the PHI test of the new species and closely related species using both LogDet transformation and splits' decomposition. The new strains are in red font, and "T" indicates holotype or ex-type strains.

macronematous, branched conidiophores, while *P. variicolor* has macronematous and micronematous, unbranched conidiophores. *Periconia xishuangbannaensis* also has a smaller size range of conidia (4.5–7 µm vs. 7.5–9.5 µm) than *P. variicolor* (Cantrell et al. 2007). In addition, pairwise nucleotide comparisons showed that ITS of *Periconia xishuangbannaensis* (GZCC 25-0677) was significantly different from that of *P. variicolor* (SACCR-64) (43/540 bp, 7.96%, with gaps) and *P. guangxiense* (GZAAS 25-0735) (38/508 bp, 7.5%, with gaps). The PHI test revealed no significant recombination event between our strains (GZCC 25-0677 and GZCC 25-0703) and the closely related taxa. The significant recombination between our two strains indicates that they are conspecific (Φw = 0.98) (Fig. 4). Therefore, *Periconia xishuangbannaensis* is introduced as a new species.

Discussion and conclusion

In this study, we introduce two new saprobic *Periconia* species, underscoring the role of unique habitats in shaping fungal diversity and advancing the taxonomic delimitation of the genus *Periconia*. Both new species lack sexual morphs, a trait consistent with most *Periconia* taxa, in which asexual states predominate. The conidiogenesis and verruculose conidia of *P. guangxiense* and *P. xishuangbannaensis* align with the generic characteristics of *Periconia* (Ellis 1971), while their conidiophores exhibit significant differences: micronematous and branched in *P. guangxiense*, versus macronematous and unbranched in *P. xishuangbannaensis*, serving as diagnostic features for species-level differentiation. The 7.8% ITS sequence divergence between *P. guangxiense* and its sister species *P. variicolor* exceeds the typical threshold for fungal species delimitation (Jeewon 2016).

Periconia species are predominantly terrestrial, functioning as saprobes or plant pathogens, with only a few documented aquatic taxa (e.g., *P. aquatica*, *P. dujuanhuensis*, *P. hongheensis*, *P. hydei*, *P. submersa*, and *P. yunnanensis*) (Dong et al. 2020; Shen et al. 2024; Hongsanan et al. 2025). The discovery of *P. guangxiense* in freshwater habitats expands the known ecological range of the genus and suggests that fungal diversity in freshwater ecosystems remains underexplored.

Periconia xishuangbannaensis formed an independent lineage in our phylogenetic analyses, but this placement received no statistical support (Fig. 1). This uncertainty underscores the potential impact of expanded taxon sampling and the inclusion of additional protein-coding markers. These measures can significantly improve phylogenetic resolution and stabilize the topological structure within Periconiaceae. Future studies, with their focus on multigene approaches incorporating more conserved loci, hold the promise of better resolving interspecific relationships within this morphologically diverse genus, inspiring further research in the field.

After 2020, there has been a notable increase in new *Periconia* species discoveries across various provinces/regions in China based on both morphology and phylogenetic analyses. In Sichuan, eight new species of *Periconia* were identified (*P. penniseti*, *P. spodiopogonis*, *P. imperatae*, *P. sichuanensis*, *P. chengduensis*, *P. cynodontis*, *P. festucae*, and *P. muchuanensis*) (Xu et al. 2022; Su et al. 2023; Yu et al. 2024); in Guizhou, *P dicranopteridis* was introduced by Bao et al. (2025); a rich haul of new taxa, including *P. artemisiae*, *P. chimonanthi*, *P. hydei*, *P. kunmingensis*, *P. pseudobyssoides*, *P. yantingensis*, and *P. yunnanensis* were introduced from Yunnan (Yang et al. 2022; Phookamsak et al. 2024; Shen

et al. 2024; Wang et al. 2024; Hongsanan et al. 2025); in Taiwan, *P. alishanica* and *P. celtidis* were reported (Tennakoon et al. 2021); in Xizang, *P. motuoensis*, *P. shannanensis*, and *P. linzhiensis* were discovered (He et al. 2025; Sun et al. 2025); and in Guangdong, *P. endophytica*, *P. wurfbainiae*, and *P. yangjiangensis* were identified (Liao et al. 2024). These discoveries collectively demonstrate that *Periconia* exhibits remarkable species diversity and a wide distribution across China. Together with the 24 new species described worldwide between 2020 and 2025, they underscore both the genus's underexplored diversity and the critical need for continued taxonomic and ecological studies.

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Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

Use of AI

No use of AI was reported.

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Author contributions

Conceptualization: TXG. Data curation: TXG, BDF. Formal analysis: SCK. Funding acquisition: TXG, BDF, SCK, SH. Investigation: SCK, ST, TXG. Methodology: SCK, ST, BDF. Project adminis-

tration: ST, TXG. Resources: TXG. Software: TXG. Validation: SCK, HJJ, ST, LYZ. Visualization: HJJ. Writing – original draft: TXG. Writing – review and editing: BDF, SCK, ST, TXG, SH.

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Data availability

All of the data that support the findings of this study are available in the main text.

References

Bao DF, Zhang JY, Lu YZ, Tian XG, Hyde KD, Liu NG, Xiao YP, Luo ZL, Karunarathna SC, Samarakoon MC, Xiao XJ, Ma J, Yang Y, Han JJ, Zhao GL, He ZJ, Wen TC, Liu ZH, Kang JC (2025) Endophytic fungi associated with medicinal ferns in Guizhou Province, China I: Morpho-molecular characterization of culturable endophytic fungi associated with *Dicranopteris* spp. Mycosphere: Journal of Fungal Biology 16(1): 2259–2455. https://doi.org/10.5943/mycosphere/16/1/13

Bruen TC, Philippe H, Bryant D (2006) A simple and robust statistical test for detecting the presence of recombination. Genetics 172(4): 2665–2681. https://doi.org/10.1534/genetics.105.048975

Cantrell S, Hanlin R, Emiliano A (2007) *Periconia variicolor* sp. nov., a new species from Puerto Rico. Mycologia 99(3): 482–487. https://doi.org/10.3852/mycologia.99.3.482

Capella-Gutiérrez S, Silla-Martínez JM, Gabaldón T (2009) trimAl: A tool for automated alignment trimming in large-scale phylogenetic analyses. Bioinformatics (Oxford, England) 25(15): 1972–1973. https://doi.org/10.1093/bioinformatics/btp348

Chethana KWT, Manawasinghe IS, Hurdeal VG, Bhunjun CS, Appadoo MA, Gentekaki E, Raspé O, Promputtha I, Hyde KD (2021) What are fungal species and how to delineate them? Fungal Diversity 109(1): 1–25. https://doi.org/10.1007/s13225-021-00483-9

Dissanayake A, Bhunjun C, Maharachchikumbura S, Liu J (2020) Applied aspects of methods to infer phylogenetic relationships amongst fungi. Mycosphere: Journal of Fungal Biology 11(1): 2652–2676. https://doi.org/10.5943/mycosphere/11/1/18

Dong W, Wang B, Hyde KD, McKenzie EH, Raja HA, Tanaka K, Abdel-Wahab MA, Abdel-Aziz FA, Doilom M, Phookamsak R (2020) Freshwater dothideomycetes. Fungal Diversity 105(1): 319–575. https://doi.org/10.1007/s13225-020-00463-5

Ellis MB (1971) Dematiaceous hyphomycetes. Commonwealth Mycological Institute, Kew. https://doi.org/10.1079/9780851986180.0000

Gunasekaran R, Janakiraman D, Rajapandian SGK, Appavu SP, Namperumalsamy Venkatesh P, Prajna L (2021) *Periconia* species - An unusual fungal pathogen causing mycotic keratitis. Indian Journal of Medical Microbiology 39(1): 36–40. https://doi.org/10.1016/j.ijmmb.2020.10.006

He SC, Hyde KD, Jayawardena RS, Thiyagaraja V, Wanasinghe DN, Zhao YW, Wang ZY, Cai T, Yang YY, Al-Otibi F, Yang Z, Zhao Q (2025) Taxonomic contributions to Pleosporales

and Kirschsteiniotheliales from the Xizang Autonomous Region, China. Mycology 1–38. https://doi.org/10.1080/21501203.2025.2493072

Hongsanan S, Khuna S, Manawasinghe I, Tibpromma S, Chethana K, Xie N, Bagacay J, Calabon M, Chen C, Doilom M (2025) Mycosphere Notes 521–571: A special edition of fungal biodiversity to celebrate Kevin D. Hyde's 70th birthday and his exceptional contributions to Mycology. Mycosphere 16(2): 2002–2180. https://doi.org/10.5943/mycosphere/16/2/1

Huelsenbeck JP, Ronquist F (2001) MRBAYES: Bayesian inference of phylogenetic trees. Bioinformatics (Oxford, England) 17(8): 754–755. https://doi.org/10.1093/bioinformatics/17.8.754

Hyde KD, Jones EBG, Liu JK, Ariyawansa H, Boehm E, Boonmee S, Braun U, Chomnunti P, Crous PW, Dai DQ, Diederich P, Dissanayake A, Doilom M, Doveri F, Hongsanan S, Jayawardena R, Lawrey JD, Li YM, Liu YX, Lücking R, Monkai J, Muggia L, Nelsen MP, Pang KL, Phookamsak R, Senanayake IC, Shearer CA, Suetrong S, Tanaka K, Thambugala KM, Wijayawardene NN, Wikee S, Wu HX, Zhang Y, Aguirre-Hudson B, Alias SA, Aptroot A, Bahkali AH, Bezerra JL, Bhat DJ, Camporesi E, Chukeatirote E, Gueidan C, Hawksworth DL, Hirayama K, De Hoog S, Kang JC, Knudsen K, Li WJ, Li XH, Liu ZY, Mapook A, McKenzie EHC, Miller AN, Mortimer PE, Phillips AJL, Raja HA, Scheuer C, Taylor JE, Tian Q, Tibpromma S, Wanasinghe DN, Wang Y, Xu JC, Yacharoen S, Yan JY, Zhang M (2013) Families of Dothideomycetes. Fungal Diversity 63(1): 1–313. https://doi.org/10.1007/s13225-013-0263-4

Index Fungorum (2025) Index Fungorum. http://www.indexfungorum.org [Accessed on August 20, 2025]

Jeewon R (2016) Establishing species boundaries and new taxa among fungi: Recommendations to resolve taxonomic ambiguities. Mycosphere: Journal of Fungal Biology 7(11): 1669–1677. https://doi.org/10.5943/mycosphere/7/11/4

Katoh K, Standley DM (2013) MAFFT Multiple Sequence Alignment Software Version 7: Improvements in Performance and Usability. Molecular Biology and Evolution 30(4): 772–780. https://doi.org/10.1093/molbev/mst010

Knapp DG, Kovács GM, Zajta E, Groenewald JZ, Crous PW (2015) Dark septate endophytic pleosporalean genera from semiarid areas. Persoonia 35(1): 87–100. https://doi.org/10.3767/003158515X687669

Kolomiets T, Pankratova L, Mukhina Z, Kassanelly D, Matveeva T, Bogomaz D, Berner D (2008) First report of leaf spot caused by *Periconia igniaria* on yellow starthistle in Russia. Plant Disease 92(6): 983–983. https://doi.org/10.1094/PDIS-92-6-0983A

Liao C, Hyde KD, Thilini Chethana KW, Dong W, Yang Y, Doilom M (2024) Three New *Periconia* species isolated from *Wurfbainia villosa* in Guangdong, China: A discussion on the doubtful taxa Clustering in this Genus. Diversity 16(3): 141. https://doi.org/10.3390/d16030141

Liu JK, Hyde KD, Jeewon R, Phillips AJL, Maharachchikumbura SSN, Ryberg M, Liu ZY, Zhao Q (2017) Ranking higher taxa using divergence times: A case study in Dothideomycetes. Fungal Diversity 84(1): 75–99. https://doi.org/10.1007/s13225-017-0385-1

Madagammana AD, Phukhamsakda C, Bhunjun CS, Rathnayaka AR, Bhat DJ, Alotibi F, Hyde KD (2024) Novel hosts, geographical records, and a global checklist of molecularly confirmed *Periconia* species. Phytotaxa 674(1): 18–54. https://doi.org/10.11646/phytotaxa.674.1.2

Miller MA, Pfeiffer W, Schwartz T (2010) Creating the CIPRES Science Gateway for inference of large phylogenetic trees. Gateway Computing Environments Workshop (GCE), New Orleans, LA, USA, 1–8. https://doi.org/10.1109/GCE.2010.5676129

Nannizzi A (1934) Repertorio sistematico dei miceti dell'uomo e degli animali. 4: 1–557.

Numata A, Iritani M, Yamada T, Minoura K, Matsumura E, Yamori T, Tsuruo T (1997) Novel antitumour metabolites produced by a fungal strain from a sea hare. Tetrahedron Letters 38(47): 8215–8218. https://doi.org/10.1016/S0040-4039(97)10198-8

Nylander J (2004) MrModeltest v2 Program Distributed by the Author. Evolutionary Biology Centre, Uppsala University, Sweden.

Phookamsak R, Hongsanan S, Bhat DJ, Wanasinghe DN, Promputtha I, Suwannarach N, Kumla J, Xie N, Dawoud TM, Mortimer PE, Xu JC, Lumyong S (2024) Exploring ascomycete diversity in Yunnan II: Introducing three novel species in the suborder Massarineae (Dothideomycetes, Pleosporales) from fern and grasses. MycoKeys 104: 9–50. https://doi.org/10.3897/mycokeys.104.112149

Rambaut A (2012) FigTree v1. 3.1: Tree figure drawing tool. FigTree v1. 3.1: Tree figure drawing tool. Edinburgh, UK.

Rannala B, Yang Z (1996) Probability distribution of molecular evolutionary trees: A new method of phylogenetic inference. Journal of Molecular Evolution 43(3): 304–311. https://doi.org/10.1007/BF02338839

Rathnayaka AR, Tennakoon DS, Jones GE, Wanasinghe DN, Bhat DJ, Priyashantha AH, Stephenson SL, Tibpromma S, Karunarathna SC (2025) Significance of precise documentation of hosts and geospatial data of fungal collections, with an emphasis on plant-associated fungi. New Zealand Journal of Botany 63(2–3): 462–489. https://doi.org/10.1080/0028825X.2024.2381734

Sarkar T, Chakraborty P, Karmakar A, Saha A, Saha D (2019) First report of *Periconia macrospinosa* causing leaf necrosis of pointed gourd in India. Journal of Plant Pathology 101(4): 1281–1281. https://doi.org/10.1007/s42161-019-00348-w

Senanayake I, Rathnayaka A, Marasinghe D, Calabon M, Gentekaki E, Lee H, Hurdeal V, Pem D, Dissanayake L, Wijesinghe S (2020) Morphological approaches in studying fungi: Collection, examination, isolation, sporulation and preservation. Mycosphere: Journal of Fungal Biology 11(1): 2678–2754. https://doi.org/10.5943/mycosphere/11/1/20

Shen H, Luo Z, Bao D, Luan S, Bhat D, Boonmee S, Wang W, Su X, Li Y, Al-Otibi F (2024) Lignicolous freshwater fungi from China IV: Morphology and phylogeny reveal new species of Pleosporales from plateau lakes in Yunnan Province, China. Mycosphere: Journal of Fungal Biology 15(1): 6439–6524. https://doi.org/10.5943/mycosphere/15/1/28

Stamatakis A, Hoover P, Rougemont J (2008) A rapid Bootstrap algorithm for the RAxML web servers. Systematic Biology 7(5): 758–771. https://doi.org/10.1080/10635150802429642

Su P, Lu Z, Tian W, Chen Y, Maharachchikumbura SSN (2023) Six additions to the genus *Periconia* (Dothideomycetes: Periconiaceae) from graminaceous plants in China. Journal of Fungi (Basel, Switzerland) 9(3): 300. https://doi.org/10.3390/jof9030300

Sun BB, He SC, Yu FM, Li CJY, Yang YY, Wang JR, Zhao Q (2025) A new species of *Periconia* (Periconiaceae, Pleosporales) from Xizang, China. Phytotaxa 93(2): 133–145. https://doi.org/10.11646/phytotaxa.693.2.2

Tanaka K, Hirayama K, Yonezawa H, Sato G, Toriyabe A, Kudo H, Hashimoto A, Matsumura M, Harada Y, Kurihara Y, Shirouzu T, Hosoya T (2015) Revision of the Massarineae (Pleosporales, Dothideomycetes). Studies in Mycology 2(1): 75–136. https://doi.org/10.1016/j.simyco.2015.10.002

Tennakoon DS, Kuo CH, Maharachchikumbura SSN, Thambugala KM, Gentekaki E, Phillips AJL, Bhat DJ, Wanasinghe DN, de Silva NI, Promputtha I, Hyde KD (2021) Taxonomic and phylogenetic contributions to *Celtis formosana*, *Ficus ampelas*,

F. septica, *Macaranga tanarius*, and *Morus australis* leaf litter inhabiting microfungi. Fungal Diversity 08(1): 1–215. https://doi.org/10.1007/s13225-021-00474-w

Tian XG, Tibpromma S, Karunarathna SC, Dai DQ, Bao DF, Mapook A, Jayawardena RS (2022) Additions to the genus *Periconia* from northern Thailand. Phytotaxa 555(1): 73–86. https://doi.org/10.11646/phytotaxa.555.1.5

Tian XG, Bao DF, Karunarathna S, Jayawardena R, Hyde K, Bhat D, Luo ZL, Elgorban A, Hongsanan S, Rajeshkumar K (2024) Taxonomy and phylogeny of ascomycetes associated with selected economically important monocotyledons in China and Thailand. Mycosphere: Journal of Fungal Biology 15(1): 1–274. https://doi.org/10.5943/mycosphere/15/1/1

Tode HJ (1791) Fvngi Mecklenbvrgenses selecti. Apudioh Fried Gvil Lemke. https://doi.org/10.5962/bhl.title.148599

Vilgalys R, Hester M (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptoc occus* species. Journal of Bacteriology 172(8): 4238–4246. https://doi.org/10.1128/jb.172.8.4238-4246.1990

Wang W, Hyde K, Bao D, Wanasinghe D, Lin C, Shen H, Lu Y, Zhang Z, Su X, Li Y (2024) Lignicolous freshwater fungi from karst landscapes in Yunnan Province, China. Mycosphere: Journal of Fungal Biology 15(1): 6525–6640. https://doi.org/10.5943/mycosphere/15/1/29

White TJ, Bruns TD, Lee S, Taylor J (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ, White TJ (Eds) PCR Protocols, a Guide to Methods and Applications. Academic Press, San Diego, 315–322. https://doi.org/10.1016/B978-0-12-372180-8.50042-1

Xu XL, Wang FH, Liu C, Yang HB, Zeng Z, Wang BX, Liu YG, Yang CL (2022) Morphology and phylogeny of ascomycetes associated with walnut trees (*Juglans regia*) in Sichuan Province, China. Frontiers in Microbiology 13: 1016548. https://doi.org/10.3389/fmicb.2022.1016548

Yang EF, Phookamsak R, Jiang HB, Tibpromma S, Bhat DJ, Karunarathna SC, Dai DQ, Xu JC, Promputtha I (2022) Taxonomic reappraisal of Periconiaceae with the description of three new *Periconia* species from China. Journal of Fungi (Basel, Switzerland) 8(3): 243. https://doi.org/10.3390/jof8030243

Yu X, Zhang S, Liang X, Zhu J, Hyde K, Liu J (2024) Bambusicolous fungi from Southwestern China. Mycosphere: Journal of Fungal Biology 15(1): 5038–5145. https://doi.org/10.5943/mycosphere/15/1/24

Zhang Y, Fournier J, Crous PW, Pointing SB, Hyde KD (2009) Phylogenetic and morphological assessment of two new species of *Amniculicola* and their allies (Pleosporales). Persoonia 23(1): 48–54. https://doi.org/10.3767/003158509X472187

Zhaxybayeva O, Gogarten JP (2002) Bootstrap, Bayesian probability and maximum likelihood mapping: Exploring new tools for comparative genome analyses. BMC Genomics 3(1): 4. https://doi.org/10.1186/1471-2164-3-4